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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/519,665

DATE: 03/27/2000
TIME: 14:49:32

Input Set: I519665.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

PS

ENTERED

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1  <110> APPLICANT: Hinrichs, Steven H.
2  <120> TITLE OF INVENTION: Methods and Compositions for Modulation of
3      Transcription Factor Activity
4  <130> FILE REFERENCE: N1374007
5  <140> CURRENT APPLICATION NUMBER: US/09/519,665
6  <141> CURRENT FILING DATE: 2000-03-06
7  <150> EARLIER APPLICATION NUMBER: 08/210880
8  <151> EARLIER FILING DATE: 1994-03-18
9  <150> EARLIER APPLICATION NUMBER: 08/881800
10 <151> EARLIER FILING DATE: 1997-06-24
11 <160> NUMBER OF SEQ ID NOS: 13
12 <170> SOFTWARE: PatentIn Ver. 2.1
13 <210> SEQ ID NO 1
14 <211> LENGTH: 271
15 <212> TYPE: PRT
16 <213> ORGANISM: Homo sapiens
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18   Met Glu Asp Ser His Lys Ser Thr Thr Ser Glu Thr Ala Pro Gln Pro
19       1             5             10             15
20   Gly Ser Ala Val Gln Gly Ala His Ile Ser His Ile Ala Gln Gln Val
21               20             25             30
22   Ser Ser Leu Ser Glu Ser Glu Glu Ser Gln Asp Ser Ser Asp Ser Ile
23               35             40             45
24   Gly Ser Ser Gln Lys Ala His Gly Ile Leu Ala Arg Arg Pro Ser Tyr
25       50             55             60
26   Arg Lys Ile Leu Lys Asp Leu Ser Ser Glu Asp Thr Arg Gly Arg Lys
27       65             70             75             80
28   Gly Asp Gly Glu Asn Ser Gly Val Ser Ala Ala Val Thr Ser Met Ser
29               85             90             95
30   Val Pro Thr Pro Ile Tyr Gln Thr Ser Ser Gly Gln Tyr Ile Ala Ile
31               100            105            110
32   Ala Pro Asn Gly Ala Leu Gln Leu Ala Ser Pro Gly Thr Asp Gly Val
33       115            120            125
34   Gln Gly Leu Gln Thr Leu Thr Met Thr Asn Ser Gly Ser Thr Gln Gln
35       130            135            140
36   Gly Thr Thr Ile Leu Gln Tyr Ala Gln Thr Ser Asp Gly Gln Gln Ile
37       145            150            155            160
38   Leu Val Pro Ser Asn Gln Val Val Val Gln Thr Ala Ser Gly Asp Met
39               165            170            175
40   Gln Thr Tyr Gln Ile Arg Thr Thr Pro Ser Ala Thr Ser Leu Pro Gln
41       180            185            190
42   Thr Val Val Met Thr Ser Pro Val Thr Leu Thr Ser Gln Thr Thr Lys
43       195            200            205
44   Thr Asp Asp Pro Gln Leu Lys Arg Glu Ile Arg Leu Met Lys Asn Arg

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45          210          215          220
46      Glu Ala Ala Arg Glu Cys Arg Arg Lys Lys Lys Glu Tyr Val Lys Cys
47      225          230          235          240
48      Leu Glu Asn Arg Val Ala Val Leu Glu Asn Gln Asn Lys Thr Leu Ile
49          245          250          255
50      Glu Glu Leu Lys Thr Leu Lys Asp Leu Tyr Ser Asn Lys Ser Val
51          260          265          270
52 <210> SEQ ID NO 2
53 <211> LENGTH: 341
54 <212> TYPE: PRT
55 <213> ORGANISM: Homo sapiens
56 <400> SEQUENCE: 2
57      Met Thr Met Glu Ser Gly Ala Glu Asn Gln Gln Ser Gly Asp Ala Ala
58          1          5          10          15
59      Val Thr Glu Ala Glu Asn Gln Gln Met Thr Val Gln Ala Gln Pro Gln
60          20          25          30
61      Ile Ala Thr Leu Ala Gln Val Ser Met Pro Ala Ala His Ala Thr Ser
62          35          40          45
63      Ser Ala Pro Thr Val Thr Leu Val Gln Leu Pro Asn Gly Gln Thr Val
64          50          55          60
65      Gln Val His Gly Val Ile Gln Ala Ala Gln Pro Ser Val Ile Gln Ser
66          65          70          75          80
67      Pro Gln Val Gln Thr Val Gln Ser Ser Cys Lys Asp Leu Lys Arg Leu
68          85          90          95
69      Phe Ser Gly Thr Gln Ile Ser Thr Ile Ala Glu Ser Glu Asp Ser Gln
70          100          105          110
71      Glu Ser Val Asp Ser Val Thr Asp Ser Gln Lys Arg Arg Glu Ile Leu
72          115          120          125
73      Ser Arg Arg Pro Ser Tyr Arg Lys Ile Leu Asn Asp Leu Ser Ser Asp
74          130          135          140
75      Ala Pro Gly Val Pro Arg Ile Glu Glu Glu Lys Ser Glu Glu Glu Thr
76          145          150          155          160
77      Ser Ala Pro Ala Ile Thr Thr Val Thr Val Pro Thr Pro Ile Tyr Gln
78          165          170          175
79      Thr Ser Ser Gly Gln Tyr Ile Ala Ile Thr Gln Gly Gly Ala Ile Gln
80          180          185          190
81      Leu Ala Asn Asn Gly Thr Asp Gly Val Gln Gly Leu Gln Thr Leu Thr
82          195          200          205
83      Met Thr Asn Ala Ala Ala Thr Gln Pro Gly Thr Thr Ile Leu Gln Tyr
84          210          215          220
85      Ala Gln Thr Thr Asp Gly Gln Gln Ile Leu Val Pro Ser Asn Gln Val
86      225          230          235          240
87      Val Val Gln Ala Ala Ser Gly Asp Val Gln Thr Tyr Gln Ile Arg Thr
88          245          250          255
89      Ala Pro Thr Ser Thr Ile Ala Pro Gly Val Val Met Ala Ser Ser Pro
90          260          265          270
91      Ala Leu Pro Thr Gln Pro Ala Glu Glu Ala Ala Arg Lys Arg Glu Val
92          275          280          285
93      Arg Leu Met Lys Asn Arg Glu Ala Ala Arg Glu Cys Arg Arg Lys Lys
94          290          295          300

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95   Lys Glu Tyr Val Lys Cys Leu Glu Asn Arg Val Ala Val Leu Glu Asn
96   305                      310                      315                      320
97   Gln Asn Lys Thr Leu Ile Glu Glu Leu Lys Ala Leu Lys Asp Leu Tyr
98                      325                      330                      335
99   Cys His Lys Ser Asp
100                      340
101  <210> SEQ ID NO 3
102  <211> LENGTH: 281
103  <212> TYPE: PRT
104  <213> ORGANISM: Saccharomyces cerevisiae
105  <400> SEQUENCE: 3
106   Met Ser Glu Tyr Gln Pro Ser Leu Phe Ala Leu Asn Pro Met Gly Phe
107   1                      5                      10                      15
108   Ser Pro Leu Asp Gly Ser Lys Ser Thr Asn Glu Asn Val Ser Ala Ser
109                      20                      25                      30
110   Thr Ser Thr Ala Lys Pro Met Val Gly Gln Leu Ile Phe Asp Lys Phe
111                      35                      40                      45
112   Ile Lys Thr Glu Glu Asp Pro Ile Ile Lys Gln Asp Thr Pro Ser Asn
113                      50                      55                      60
114   Leu Asp Phe Asp Phe Ala Leu Pro Gln Thr Ala Thr Ala Pro Asp Ala
115                      65                      70                      75                      80
116   Lys Thr Val Leu Pro Ile Pro Glu Leu Asp Asp Ala Val Val Glu Ser
117                      85                      90                      95
118   Phe Phe Ser Ser Ser Thr Asp Ser Thr Pro Met Phe Glu Tyr Glu Asn
119                      100                     105                     110
120   Leu Glu Asp Asn Ser Lys Glu Trp Thr Ser Leu Phe Asp Asn Asp Ile
121                      115                     120                     125
122   Pro Val Thr Thr Asp Asp Val Ser Leu Ala Asp Lys Ala Ile Glu Ser
123                      130                     135                     140
124   Thr Glu Glu Val Ser Leu Val Pro Ser Asn Leu Glu Val Ser Thr Thr
125                      145                     150                     155                     160
126   Ser Phe Leu Pro Thr Pro Val Leu Glu Asp Ala Lys Leu Thr Gln Thr
127                      165                     170                     175
128   Arg Lys Val Lys Lys Pro Asn Ser Val Val Lys Lys Ser His His Val
129                      180                     185                     190
130   Gly Lys Asp Asp Glu Ser Arg Leu Asp His Leu Gly Val Val Ala Tyr
131                      195                     200                     205
132   Asn Arg Lys Gln Arg Ser Ile Pro Leu Ser Pro Ile Val Pro Glu Ile
133                      210                     215                     220
134   Asp Asp Pro Ala Ala Leu Lys Arg Ala Arg Asn Thr Glu Ala Ala Arg
135                      225                     230                     235                     240
136   Arg Ser Arg Ala Arg Lys Leu Gln Arg Met Lys Gln Leu Glu Asp Lys
137                      245                     250                     255
138   Val Glu Glu Leu Leu Ser Lys Asn Tyr His Leu Glu Asn Glu Val Ala
139                      260                     265                     270
140   Arg Leu Lys Lys Leu Val Gly Glu Arg
141                      275                     280
142  <210> SEQ ID NO 4
143  <211> LENGTH: 27
144  <212> TYPE: DNA

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145 <213> ORGANISM: Artificial Sequence
146 <220> FEATURE:
147 <223> OTHER INFORMATION: Description of Artificial Sequence:
148     Oligonucleotide
149 <400> SEQUENCE: 4
150     agagattgcc tgacgtcaga gagctag                27
151 <210> SEQ ID NO 5
152 <211> LENGTH: 21
153 <212> TYPE: DNA
154 <213> ORGANISM: Artificial Sequence
155 <220> FEATURE:
156 <223> OTHER INFORMATION: Description of Artificial Sequence:
157     Oligonucleotide
158 <400> SEQUENCE: 5
159     cgcttgatga gtcagccgga a                21
160 <210> SEQ ID NO 6
161 <211> LENGTH: 30
162 <212> TYPE: DNA
163 <213> ORGANISM: Artificial Sequence
164 <220> FEATURE:
165 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
166 <400> SEQUENCE: 6
167     gactagatga gagctactct aagaggaacg        30
168 <210> SEQ ID NO 7
169 <211> LENGTH: 94
170 <212> TYPE: PRT
171 <213> ORGANISM: Artificial Sequence
172 <220> FEATURE:
173 <223> OTHER INFORMATION: Description of Artificial Sequence: Protein
174 <400> SEQUENCE: 7
175     Gln Val Lys Leu Gln Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
176         1             5             10             15
177     Ser Trp Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Glu
178             20             25             30
179     Gly Met His Trp Val Arg Gln Ala Pro Glu Lys Gly Leu Glu Trp Val
180             35             40             45
181     Ala Tyr Ile Ser Ser Gly Ser Ser Thr Leu His Tyr Ala Asp Thr Val
182             50             55             60
183     Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Pro Lys Asn Thr Leu Phe
184             65             70             75             80
185     Leu Gln Met Lys Leu Pro Ser Leu Cys Tyr Gly Leu Leu Gly
186             85             90
187 <210> SEQ ID NO 8
188 <211> LENGTH: 107
189 <212> TYPE: PRT
190 <213> ORGANISM: Artificial Sequence
191 <220> FEATURE:
192 <223> OTHER INFORMATION: Description of Artificial Sequence: Protein
193 <400> SEQUENCE: 8
194     Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile

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195          1          5          10          15
196      Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Met
197          20          25          30
198      Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Phe
199          35          40          45
200      Gly Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg Phe Thr Gly Ser
201          50          55          60
202      Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu Glu
203          65          70          75          80
204      Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu Asp Pro Phe Thr
205          85          90          95
206      Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg
207          100          105
208      <210> SEQ ID NO 9
209      <211> LENGTH: 15
210      <212> TYPE: PRT
211      <213> ORGANISM: Artificial Sequence
212      <220> FEATURE:
213      <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide
214      Internal Fragment
215      <400> SEQUENCE: 9
216      Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
217          1          5          10          15
218      <210> SEQ ID NO 10
219      <211> LENGTH: 11
220      <212> TYPE: PRT
221      <213> ORGANISM: Artificial Sequence
222      <220> FEATURE:
223      <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide
224      <220> FEATURE:
225      <221> NAME/KEY: SITE
226      <222> LOCATION: (1)
227      <223> OTHER INFORMATION: This is an acidic amino acid.
228      <220> FEATURE:
229      <221> NAME/KEY: SITE
230      <222> LOCATION: (2)
231      <223> OTHER INFORMATION: This is an acidic amino acid.
232      <220> FEATURE:
233      <221> NAME/KEY: SITE
234      <222> LOCATION: (3)..(5)
235      <223> OTHER INFORMATION: Positions 3-5 represent a total of 2 or 3 amino
236      acid residues and these can be any amino acid
237      residues.
238      <220> FEATURE:
239      <221> NAME/KEY: SITE
240      <222> LOCATION: (6)
241      <223> OTHER INFORMATION: This amino acid is either leucine or arginine.
242      <220> FEATURE:
243      <221> NAME/KEY: SITE
244      <222> LOCATION: (9)..(10)

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Input Set: I519665.RAW

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249	W "N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Xaa Xaa Lys Arg Xaa Xaa A
291	W "N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa X
293	W "N" or "Xaa" used: Feature required	Xaa Xaa Xaa Asn
353	W "N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa X
355	W "N" or "Xaa" used: Feature required	Xaa Xaa Xaa Asn Xaa Xaa Ala Arg Xaa Arg L